

SEQUENCE LISTING

<110> Arthur B. Raitano
Daniel E.H. Afar
Aya Jakobovits
Mary Faris
Rene S. Hubert
Steve Chappell Mitchell
Douglas C. Saffran

<120> NOVEL G PROTEIN-COUPLED RECEPTOR
UP-REGULATED IN PROSTATE CANCER AND USES THEREOF

<130> 129.24USU1

<150> 60/157,902

<151> 1999-10-05

<160> 50

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3136

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (133)...(1083)

<400> 1

cagagaggct gtatttcagt gcagcctgcc agacctcttc tggaggaaga ctggacaaaag	60
ggggtcacac attccttcca tacggttgag cctctacctg cctggtgctg gtcacagttc	120
agcttcttca tg atg gtg gat ccc aat ggc aat gaa tcc agt gct aca tac	171
Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr	
1 5 10	

ttc atc cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg	219
Phe Ile Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu	
15 20 25	

gcc ttc cca ttg tgc tcc ctc tac ctt att gct gtg cta ggt aac ttg	267
Ala Phe Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu	
30 35 40 45	

aca atc atc tac att gtg cgg act gag cac agc ctg cat gag ccc atg	315
Thr Ile Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met	
50 55 60	

tat ata ttt ctt tgc atg ctt tca ggc att gac atc ctc atc tcc acc	363
Tyr Ile Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr	
65 70 75	

tca tcc atg ccc aaa atg ctg gcc atc ttc tgg ttc aat tcc act acc	411
Ser Ser Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr	
80 85 90	

atc cag ttt gat gct tgt ctg cta cag att ttt gcc atc cac tcc tta	459
Ile Gln Phe Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu	
95 100 105	

tct ggc atg gaa tcc aca gtg ctg ctg gcc atg gct ttt gac cgc tat	507
Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr	
110 115 120 125	
gtg gcc atc tgt cac cca ctg cgc cat gcc aca gta ctt acg ttg cct	555
Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro	
130 135 140	
cgt gtc acc aaa att ggt gtg gct gct gtg gtg cgg ggg gct gca ctg	603
Arg Val Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu	
145 150 155	
atg gca ccc ctt cct gtc ttc atc aag cag ctg ccc ttc tgc cgc tcc	651
Met Ala Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser	
160 165 170	
aat atc ctt tcc cat tcc tac tgc cta cac caa gat gtc atg aag ctg	699
Asn Ile Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu	
175 180 185	
gcc tgt gat gat atc cgg gtc aat gtc gtc tat ggc ctt atc gtc atc	747
Ala Cys Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile	
190 195 200 205	
atc tcc gcc att ggc ctg gac tca ctt ctc atc tcc ttc tca tat ctg	795
Ile Ser Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu	
210 215 220	
ctt att ctt aag act gtg ttg ggc ttg aca cgt gaa gcc cag gcc aag	843
Leu Ile Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys	
225 230 235	
gca ttt ggc act tgc gtc tct cat gtg tgt gct gtg ttc ata ttc tat	891
Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr	
240 245 250	
gta cct ttc att gga ttg tcc atg gtg cat cgc ttt agc aag cgg cgt	939
Val Pro Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg	
255 260 265	
gac tct ccg ctg ccc gtc atc ttg gcc aat atc tat ctg ctg gtt cct	987
Asp Ser Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro	
270 275 280 285	
cct gtg ctc aac cca att gtc tat gga gtg aag aca aag gag att cga	1035
Pro Val Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg	
290 295 300	
cag cgc atc ctt cga ctt ttc cat gtg gcc aca cac gct tca gag ccc	1083
Gln Arg Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro	
305 310 315	
taggtgtcag tgatcaaaact tcttttccat tcagagtcct ctgattcaga ttttaattgtt	1143
aacatttttg aagacagtat tcagaaaaaa aatttcctta ataaaaaata caactcagat	1203
ccttcaaaata tgaaactggg tggggaatct ccattttttc aatattattt tcttctttgt	1263
tttcttgcta catataatta ttaataccct gactagggttg tggttgagg gttattactt	1323
ttcattttac catgcagtcc aaatctaaac tgcttctact gatggtttac agcattctga	1383
gataagaatg gtacatctag agaacatttg ccaaaggcct aagcacggca aaggaaaata	1443
aacacagaat ataataaaat gagataatct agcttaaaac tataacttcc tcttcagaac	1503
tcccaaccac attggatctc agaaaaatgc tgtcttcaaa atgacttcta cagagaagaa	1563
ataatttttc ctctggacac tagcacttaa ggggaagatt ggaagtaaag ccttgaaaag	1623
agtacattta cctacgttaa tgaaagttga cacactgttc tgagagtttt cacagcatat	1683

```

ggaccctgtt tttcctatatt aattttctta tcaacccttt aattaggcaa agatattatt 1743
agtaccctca ttgtagccat gggaaaattg atgttcagt gggatcagt aattaaatgg 1803
ggtcatataa gtataaaaaa taataaaaaa aaagacttca tgcccaatct catatgatgt 1863
ggaagaactg ttagagagac caacagggtg gtgggttaga gatttccaga gtcttacatt 1923
ttctagagga ggtatttaat ttcttctcac tcatccagt ttgtatttag gaatttcctg 1983
gcaacagaac tcatggcttt aatcccacta gctattgctt attgtcctgg tccaattgcc 2043
aattacctgt gtcttgggaag aagtgatttc taggttcacc attatggaag attcttattc 2103
agaaagtctg catagggtct atagcaagtt atttattttt aaaagttcca taggtgattc 2163
tgataggcag tgagggttag gagccaccag ttatgatggg aagtatggaa tggcagggtct 2223
tgaagataac attggccttt tgagtgtgac tcgtagctgg aaagtgaggg aatcttcagg 2283
accatgcttt atttggggct ttgtgcagta tggaaacagg actttgagac caggaaagca 2343
atctgactta ggcattggaa tcaggcattt ttgcttctga ggggctatta ccaaggggta 2403
ataggtttca tcttcaacag gatatgacaa cagtgttaac caagaaactc aaattacaaa 2463
tactaaaaa tgtgatcata tatgtggtaa gtttcatttt ctttttcaat cctcagggttc 2523
cctgatattg attcctataa catgcttttc tccccctttg taatggatat catatttgga 2583
aatgcctatt taatacttgt atttgctgct ggactgtaag cccatgaggg cactgtttat 2643
tattgaatgt catctctgtt catcattgac tgccttttgc tcatcattga atcccccagc 2703
aaagtgccta gaacataata gtgcttatgc ttgacaccgg ttatttttca tcaaacctga 2763
ttccttctgt cctgaacaca tagccaggca attttccagc cttctttgag ttgggtatta 2823
ttaaattctg gccattactt ccaatgtgag tggaaagtac atgtgcaatt tctatactg 2883
gctcataaaa cctcccatg tgcagccttt catgttgaca taaatgtga cttgggaagc 2943
tatgtgttac acagagtaaa tcaccagaag cctggatttc tgaaaaaact gtgcagagcc 3003
aaacctctgt catttgcaac tcccacttgt atttgtacga ggcagttgga taagtgaana 3063
ataaagtact atttgtcaa gaaaaaaa aaaaaaaa aaaaaaaa aaaaaaaa 3123
aaaaaaaaaaa aaa 3136

```

```

<210> 2
<211> 317
<212> PRT
<213> Homo Sapiens

```

```

<400> 2
Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu
1 5 10 15
Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe Pro
20 25 30
Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile Ile
35 40 45
Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
50 55 60
Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser Met
65 70 75 80
Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe
85 90 95
Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu Ser Gly Met
100 105 110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
115 120 125
Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr
130 135 140
Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala Pro
145 150 155 160
Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu
165 170 175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp
180 185 190
Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser Ala
195 200 205
Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile Leu
210 215 220
Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe Gly
225 230 235 240
Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro Phe

```

245 250 255
 Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro
 260 265 270
 Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val Leu
 275 280 285
 Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg Ile
 290 295 300
 Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
 305 310 315

<210> 3
 <211> 320
 <212> PRT
 <213> Rat Protein

<400> 3
 Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Met Leu Ile Gly Ile
 1 5 10 15
 Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
 20 25 30
 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
 35 40 45
 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50 55 60
 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65 70 75 80
 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
 85 90 95
 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110
 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
 130 135 140
 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 145 150 155 160
 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175
 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
 180 185 190
 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205
 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
 210 215 220
 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255
 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
 260 265 270
 Val Leu Met Gly Asp Val Tyr Leu Leu Pro Pro Val Ile Asn Pro
 275 280 285
 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
 290 295 300
 Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
 305 310 315 320

<210> 4
 <211> 320
 <212> PRT
 <213> Homo Sapiens

<400> 4

Met Ser Ser Cys Asn Phe Thr His Ala Thr Cys Val Leu Ile Gly Ile
1 5 10 15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
20 25 30
Met Tyr Val Val Ala Met Cys Gly Asn Cys Ile Val Val Phe Ile Val
35 40 45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
50 55 60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65 70 75 80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Ile Glu Ala Cys
85 90 95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
100 105 110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
115 120 125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
130 135 140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
145 150 155 160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
165 170 175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
180 185 190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
195 200 205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
210 215 220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
225 230 235 240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
245 250 255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
260 265 270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
275 280 285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
290 295 300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
305 310 315 320

<210> 5

<211> 427

<212> DNA

<213> Homo Sapiens

<400> 5

gatcaaaactt	cttttccatt	cagagtcttc	tgattcagat	tttaatgtta	acattttgga	60
agacagtatt	cagaaaaaaa	atttccttaa	taaaaataca	actcagatcc	ttcaaatacg	120
aaactgggtg	gggaatctcc	attttttcaa	tattattttc	ttctttgttt	tcttgctacg	180
tataattatt	aatatcctga	ctaggttggtg	gttgagggtg	tattactttt	cattttacca	240
tgagtgccaa	atctaaactg	cttctactga	tggtttacag	cattctgaga	taagaatggt	300
acatctagag	aacatttgcc	aaaggcctaa	gcacagcaaa	ggaaaataaa	cacagaatat	360
aataaaatga	gataatctag	cttaaaacta	taacttcttc	tttagaactc	ccaaccacat	420
ttggatc						427

<210> 6

<211> 501

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (1)...(501)

<400> 6

```
gct gtg gcc atg ttt att gga gtg ttg gat cta ttc ttt atc atc cta      48
Ala Val Ala Met Phe Ile Gly Val Leu Asp Leu Phe Phe Ile Ile Leu
 1              5              10              15

tct tat atc ttt atc ctt cag gca gtt cta caa ctc tcc tct cag gag      96
Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln Leu Ser Ser Gln Glu
      20              25              30

gcc cgc tac aaa gca ttt ggg aca tgt gtc tct cac ata ggt gcc atc      144
Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser His Ile Gly Ala Ile
      35              40              45

tta gcc ttc tac aca cct tca gtc atc tct tca gtc atg cac cgt gtg      192
Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser Val Met His Arg Val
      50              55              60

gcc cgc tgt gct gtg cca cac gtc cac att ctc ctc gcc aat ttc tat      240
Ala Arg Cys Ala Val Pro His Val His Ile Leu Leu Ala Asn Phe Tyr
      65              70              75              80

ctg ctc ttc cca ccc atg gtc aat ccc atc atc tat ggc gtt aag acc      288
Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile Tyr Gly Val Lys Thr
      85              90              95

aag cag atc cgt gac agt ctt ggg agt att cct gag aaa gga tgt gtg      336
Lys Gln Ile Arg Asp Ser Leu Gly Ser Ile Pro Glu Lys Gly Cys Val
      100             105             110

aat aga gag tga gga ata agt gga aaa aga gtg ggg ccc agt gaa tgc      384
Asn Arg Glu * Gly Ile Ser Gly Lys Arg Val Gly Pro Ser Glu Cys
      115             120             125

tgt agt ggg cca ggg ctg tgc tga gag tag atg ggt cct aga ctc cac      432
Cys Ser Gly Pro Gly Leu Cys * Glu * Met Gly Pro Arg Leu His
      130             135             140

gtt tag ttc ttt tct tgt att atg aaa aga ata aat gat gtc ctg aag      480
Val * Phe Phe Ser Cys Ile Met Lys Arg Ile Asn Asp Val Leu Lys
      145             150             155

ctc aga aaa aaa aaa aaa aaa      501
Leu Arg Lys Lys Lys Lys Lys
      160
```

<210> 7

<211> 163

<212> PRT

<213> Homo Sapiens

<400> 7

```
Ala Val Ala Met Phe Ile Gly Val Leu Asp Leu Phe Phe Ile Ile Leu
 1              5              10              15
Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln Leu Ser Ser Gln Glu
      20              25              30
Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser His Ile Gly Ala Ile
      35              40              45
Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser Val Met His Arg Val
      50              55              60
Ala Arg Cys Ala Val Pro His Val His Ile Leu Leu Ala Asn Phe Tyr
```

65		70		75		80									
Leu	Leu	Phe	Pro	Pro	Met	Val	Asn	Pro	Ile	Ile	Tyr	Gly	Val	Lys	Thr
			85						90					95	
Lys	Gln	Ile	Arg	Asp	Ser	Leu	Gly	Ser	Ile	Pro	Glu	Lys	Gly	Cys	Val
			100					105					110		
Asn	Arg	Glu	Gly	Ile	Ser	Gly	Lys	Arg	Val	Gly	Pro	Ser	Glu	Cys	Cys
		115					120				125				
Ser	Gly	Pro	Gly	Leu	Cys	Glu	Met	Gly	Pro	Arg	Leu	His	Val	Phe	Phe
	130					135					140				
Ser	Cys	Ile	Met	Lys	Arg	Ile	Asn	Asp	Val	Leu	Lys	Leu	Arg	Lys	Lys
145				150					155					160	
Lys	Lys	Lys													

<210> 8
 <211> 14
 <212> PRT
 <213> Homo Sapiens

<400> 8
 Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe
 1 5 10

<210> 9
 <211> 13
 <212> PRT
 <213> Homo Sapiens

<400> 9
 Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu Pro
 1 5 10

<210> 10
 <211> 4
 <212> PRT
 <213> Homo Sapiens

<400> 10
 Asn Glu Ser Ser
 1

<210> 11
 <211> 4
 <212> PRT
 <213> Homo Sapiens

<400> 11
 Asn Leu Thr Ile
 1

<210> 12
 <211> 4
 <212> PRT
 <213> Homo Sapiens

<400> 12
 Asn Ser Thr Thr
 1

<210> 13
 <211> 4
 <212> PRT
 <213> Homo Sapiens

<400> 13
Arg Arg Asp Ser
1

<210> 14
<211> 4
<212> PRT
<213> Homo Sapiens

<400> 14
Ser Leu His Glu
1

<210> 15
<211> 4
<212> PRT
<213> Homo Sapiens

<400> 15
Ser Gly Ile Asp
1

<210> 16
<211> 4
<212> PRT
<213> Homo Sapiens

<400> 16
Ser Gly Met Glu
1

<210> 17
<211> 6
<212> PRT
<213> Homo Sapiens

<400> 17
Gly Asn Glu Ser Ser Ala
1 5

<210> 18
<211> 6
<212> PRT
<213> Homo Sapiens

<400> 18
Gly Leu Glu Glu Ala Gln
1 5

<210> 19
<211> 6
<212> PRT
<213> Homo Sapiens

<400> 19
Gly Met Glu Ser Thr Val
1 5

<210> 20
<211> 6
<212> PRT
<213> Homo Sapiens

<400> 20
Gly Thr Cys Val Ser His
1 5

<210> 21
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ttttgatcaa gctt 14

<210> 22
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
ctaatacgac tcactatagg gctcgagcgg ccgcccgggc ag 42

<210> 23
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
ggcccgtcct ag 12

<210> 24
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gtaatacgac tcactatagg gcagcgtggt cgcggccgag 40

<210> 25
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
cggctcctag 10

<210> 26
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 26

ctaatacgac tcactatagg gc

22

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 27

tcgagcggcc gcccgggcag ga

22

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 28

agcgtggtcg cggccgagga

20

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 29

atatacgccgc gctcgtcgtc gacaa

25

<210> 30

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30

agccacacgc agtcattgt agaagg

26

<210> 31

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 31

atcctgacta ggttggtggtt ggag

24

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 32
tgtggttggg agttctaaag agga

24

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> FLAG tag

<400> 33
gattacaagg atgacgacga taag

24

<210> 34
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 34
ccgaattcca tcttctggtt caatttc

27

<210> 35
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 35
cctctcgagt tcacatggaa aagtcgaag

29

<210> 36
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 36
Ser Leu His Glu Pro Met Tyr
1 5

<210> 37
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 37
Ala Met Ala Phe Asp Arg Tyr
1 5

<210> 38

<211> 7
<212> PRT
<213> Homo Sapiens

<400> 38
Tyr Val Ala Ile Cys His Pro
1 5

<210> 39
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 39
Lys Ala Phe Gly Thr Cys Val
1 5

<210> 40
<211> 7
<212> PRT
<213> Homo Sapiens

<400> 40
Gly Val Lys Thr Lys Glu Ile
1 5

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 41
agycncays mnccnatgta y

21

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 42
tcnctncays mnccnatgta y

21

<210> 43
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 43
agyttrcays mnccnatgta y

21

<210> 44
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 44
tcnttrcays mnccnatgta y

21

<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 45
gcnatggcnt tygaycgnta y

21

<210> 46
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(21)
<223> n = A,T,C or G

<400> 46
gcnatggcnt tygayagrta y

21

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<221> misc_feature
<222> (1)...(21)

<223> n = A,T,C or G

<400> 47

taygtngcna thtgycaycc n

21

<210> 48

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<221> misc_feature

<222> (1)...(21)

<223> n = A,T,C or G

<400> 48

nggrtgrcad atngcnacrt a

21

<210> 49

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<221> misc_feature

<222> (1)...(21)

<223> n = A,T,C or G

<400> 49

nacrcangtn ccraangcyt t

21

<210> 50

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<221> misc_feature

<222> (1)...(21)

<223> n = A,T,C or G

<400> 50

datytsyttt gtyttncnc c

21